SEQUENCE LISTING

```
(1) GENERAL INFORMATION:
 5
           (i) ANMELDER:
                (A) NAME: Vasopharm Biotech GmbH & Co. KG
                (B) STREET: Leichtackerstr. 6
                (C) CITY: Veitshöchheim
10
                (D) STATE: Bayern
                (E) COUNTRY: Deutschland
                (F) POSTAL CODE: 97209
          (ii) TITEL OF THE INVENTION: Isolated and purified human soluble
15
     guanylyl cyclase al/B1 (hsGCal/B1)
        (iii) NUMBER OF SEQUENCES: 10
20
         (iv) COMPUTER-READABLE FORM:
               (A) MEDIUM TYPE: Floppy disk
               (B) COMPUTER: IBM PC compatible
                (C) OPERATING SYSTEM: PC-DOS/MS-DOS
               (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)
25
     (2) DATA TO SEQ ID NO: 1:
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 3015 basepairs
30
               (B) TYPE: nucleotide
               (C) STRANDEDNESS: doublestrand
               (D) TOPOLOGY: linear
         (ii) MOLECULE TYPE: genomic DNA
35
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
40
     CCCTTATGGC GATTGGGCGG CTGCAGAGAC CAGGACTCAG TTCCCCTGCC CTAGTCTGAG
                                                                              60
     CCTAGTGGGT GGGACTCAGC TCAGAGTCAG TTTTCCAGAA GCAGGTTTCA GTGCAGAGTT
                                                                              120
     TTCCTACACT TTTCCTGCGC TAGAGCAGCG AGCAGCCTGG AACAGACCCA GGCGGAGGAC
                                                                           . 180
    ACCTGTGGGG GAGGGAGCGC CTGGAGGAGC TTAGAGACCC CAGCCGGGCG TGATCTCACC
     ATGTGCGGAT TTGCGAGGCG CGCCCTGGAG CTGCTAGAGA TCCGGAAGCA CAGCCCCGAG
                                                                              300
45
     GTGTGCGAAG CCACCAAGAC TGCGGCTCTT GGAGAAAGCG TGAGCAGGGG GCCACCGCGG
                                                                             360
     TCTCCGCGCC TGTCTGCACC CTGTCGCCTG AGCTGCCTGA CAGTGACAAT GACATCCCAG
                                                                             420
     TTACCAGTGT CCTTGAATTG ATAGTGGCTT CTGTTTGTCA GTCTCATATA AGAACTACAG
                                                                              480
     CTCATCAGGA GGAGATCGCA GCAGGGTAAG AGACACCAAC ACCATGTTCT GCACGAAGCT
                                                                              540
     CAAGGATCTC AAGATCACAG GAGAGTGTCC TTTCTCCTTA CTGGCACCAG GTCAAGTTCC
                                                                              600
50
     TAACGAGTCT TCAGAGGAGG CAGCAGGAAG CTCAGAGAGC TGCAAAGCAA CCGTGCCCAT
                                                                              660
     CTGTCAAGAC ATTCCTGAGA AGAACATACA AGAAAGTCTT CCTCAAAGAA AAACCAGTCG
                                                                              720
     GAGCCGAGTC TATCTTCACA CTTTGGCAGA GAGTATTTGC AAACTGATTT TCCCAGAGTT
                                                                              780
     TGAACGGCTG AATGTTGCAC TTCAGAGAAC ATTGGCAAAG CACAAAATAA AAGAAAGCAG
                                                                              840
     GAAATCTTTG GAAAGAGAAG ACTTTGAAAA AACAATTGCA GAGCAAGCAG TTGCAGCAGG
                                                                              900
55
     AGTTCCAGTG GAGGTTATCA AAGAATCTCT TGGTGAAGAG GTTTTTAAAA TATGTTACGA
                                                                              960
     GGAAGATGAA AACATCCTTG GGGTGGTTGG AGGCACCCTT AAAGATTTTT TAAACAGCTT
                                                                             1020
     CAGTACCCTT CTGAAACAGA GCAGCCATTG CCAAGAAGCA GGAAAAAGGG GCAGGCTTGA
                                                                             1080
     GGACGCCTCC ATTCTATGCC TGGATAAGGA GGATGATTTT CTACATGTTT ACTACTTCTT
                                                                             1140
     CCCTAAGAGA ACCACCTCCC TGATTCTTCC CGGCATCATA AAGGCAGCTG CTCACGTATT
                                                                            1200
60
    ATATGAAACG GAAGTGGAAG TGTCGTTAAT GCCTCCCTGC TTCCATAATG ATTGCAGCGA
     GTTTGTGAAT CAGCCCTACT TGTTGTACTC CGTTCACATG AAAAGCACCA AGCCATCCCT
                                                                            1320
     GTCCCCCAGC AAACCCCAGT CCTCGCTGGT GATTCCCACA TCGCTATTCT GCAAGACATT
```

1380

CCCTAGTGAA ATCCCCGGAA TCTGCCATTT TCTGGATGCT TACCAACAAG GAACAACTC AAAACCATGC TTCCAAAAGA AAGATGTGGA AGATGGCAAT ATCAGGAATA GATTAGCAAC CTATATACCT ATTTATAAGT CTTTGGGGTT TAGCCAACAGC AAGATGTGTA GAGCCTCTGA AAGCACTTTA GGGATTGTAG ATGGCTAACA AGCAGTATTA AAAATTCAGG AGCCAACTCA CAATCTTTCT CCTGTTTAAC ATGACAAAAT GTACTCACTT CAGGATACTCA GGTCTCTCAAG AAAAAAAAA AAACCTTAAA AAGCTACTTT TGTGGGATA TTTCTATTAT ATAACCAGCA CTTACTACCT GTACTCAAAA TCCAGCACCT TGTACAATATA TCAGGATAATT GTAGTCAATT GTACAAACTG ATGGGATCAC CTGCAATCTC ATATCCTGGT GGAATGCCAT GGTTATTAAA GTGTGTTTGT GATAGTGTCG TCAAAAAAAAAA			
AGGCTGATG AACAGCAGAGA TCTGACTCCA AAAATCAACC AGACGTTAG CGGGATCATG ACTAGGAGAA ATTGCACAT TGTGTACACA ATGACTCAA TTGTTGAATC CAGGATCATC TGTTTTTGGGGCT CAAAGCCCAA ATGACACTCAA TTGTTGAATC CAGGCACACT TTGTTTTTTGG GGTCACCCTG TGTGGACAAA ATGACTCAAA TTGTTGAATC CAGTGCAATC TTGTTTTTTGG GGTCACCCTG CAAAGCACTG AGGGATCTG TCTTAATAGG GAAACAACC CACAGCCC TGAGGAGAGGC CAAAGACAAAA ACAGTAGACC TTCTTGTGTCCT CATATTTCCC CAGACGCC TGAGGAGAGGA		TCCATTCCAT TTCATGTTTG ACAAAGATAT GACAATTCTG CAATTTGGCA ATGGCATCAG 1	440
TCTGACTCCA AMATCAACC AGACGTTTAG CGGGATCATG ACTATCTCA ATATGCAGCT TGTGTAGGA GTGAGAGAGAT GGGGACAACT TGTAGAGAGAA TCTCAAAGG TTATGCACCT CAAAGGCCAA ATGATCTACA TTGTCAAATC CAGTCCAATC CTCTCAAGGC TTGTGGACACAATCAATCAACCC CAAAGGCCAAACAACTCAAAGACAATTCAACAGACAACAACAACAACAACAACAACAACAACAACAA		AAGGCTGATG AACAGGAGAG ACTTTCAAGG AAAGCCTAAT TTTGAAGAAT ACTTTGAAAT 1	500
TGTTGTAGA GTGAGGAGAT GGGACARCTC TGTGAAGAAA TCTTCAAGGG TTATGGACCT GAAGGCCAA ATGACTCAAC TTGTGAACT CAGTCCAATC CATGCCACT TGTGACAGA TTAGAAGATT TTACAGGAC AGGGCTCTAC CTCTCAGACA TCCCAATTCA CATAGACACAC AGGGATCAGA GGGAAGAGCCT GAAGAAGACC CGAAGAGCCT GAAGAAAAAAAAAA		TCTGACTCCA AAAATCAACC AGACGTTTAG CGGGATCATG ACTATGTTGA ATATGCAGTT 1	560
S CARAGGCCAA ATGATCTACA TICTICAATC CAGTECAATC TICTITITIEG GGTCACCCTE TGGGACAGA TITGAGAGGT TITGAGAGGC CAGGCTCTAC CITCTAGACA TICCCATTCA CAATCCACTG AGGGAGCTGA AGGCTACCCT TAGGCAGCC CAGGCTCAAG GAAGAGCTG GGGAAGCTGA AGGCTACCCT TAGGCAAGCC CAGGCTCAAG GAAGAAAAAG ACAGTGAGCC TICTICTCCC CATTTTCC TETGAGCTGC CATGCTAGGG TICTACTCCCA TICTICCCCA GTGCTACCC CACAGGCCC TGGAGGGGGA CATGCTAGG TICACTCCCA TICTICCCCA GTGCTCACCC CACAGGCCC TCTCCTCCAGACACC CAATGCACTG TACACTCCT TCCACCAGCA GTGTGGACGC CACAGGCTC TACACCTCCA TGCACCCCC CAGGCTCCC CAATGCACTG CATCCCATTCCC ATGCTCACC GTGCTACCC CACAGGCTC TACACCTCC CAATGCACTG CACCCTCCAGAGAT GACCATTGCC CAATGCACTG TACACTCGCT TCCACCAGCA GTGTGAGCAC CAAGAGCACT TACACCATGCC CAATGCACTA GCGCTGATGC CCCTGAAGAT GATGGACCTC TGCATGAGAA TACCCATTGCC CCTTGGAGTT AAAATGCCC GTTACTTCTT TITTGGAAC AAAGTCACCT CACAACACT TACCCACACA ATTTGAGTC CACGGAAAAT CAATGCACTC TGCATCAAG CAATGCACACA ATTTGGATC CACGAAAAAT CAATGCACACACACACT CCCTTACTGAA AACACTCC TGGATCACAG GAGAACTC CACAACACT CCCTACTGAA ATCCCCGGAA TCTCCCATTT TCTGGATTCAT TACCAACAAG GAACCAACCT CCCTTACTGAA ATCCCCGGAA TCTCCCATTT TCTGGATTCATT TACCAACAAG GAACCACACACAC ATTCCACAACA CATTCACACAA AACACTCCAAACAACAACAACACACAACACAACACACAC		TGTTGTACGA GTGAGGAGAT GGGACAACTC TGTGAAGAAA TCTTCAAGGG TTATGGACCT 1	620
TOTGGACAGA TTAGAGACATT TACAGGACG AGGGCTCTAC CTCTCAGACA TCCCAATTCA CANTGCACTG AGGGATTGG TCTTATATAGG GGACAAGCC CGAGCTCAGA ATGGCCTGAA GAAGAGGCTG GGGAAGCTGA AGGCTACCT TGAGCAAGCC CACCATACCC TGGAGGAGGA GAAGAAAAAA ACAGTAGACC TTCTGTGTCCT CATATTCCC TGTGAGGTG CTCAGCAGGCA GACGAAAAAA ACAGTTGCACACC TTCTGTGTCCT CATATTCCC TGTGAGGTG CTCTCACACA CATCGTTGGG TTCACTCCCA TCGCCTCCCA GTGCTCACCG CTGCAGGTCA TCACCATGCC CAATCGCTTGG TACACTCGCT TCGACCAGCA GTGCTGACAGC CTGCAGGTCA TCACCATGCC GACCATTGGC GATGCCTATT GTGTAGCTGG GGGATTCAC AAAAGAGAGTG ATACTCATGC GACCATTGGC GATGCCTATT GTGTAGCTGG GGGATTCAC AAAAGAGAGTG ATACTCATGC CCATGGAAA CCTATCAAGA TGCGAATTG ACTGCACTTT GGATCAGTT TTCGTGGCGT CGTTGGAGTT AAAATGCCCC GTTACTGTT TTTTGGAAAC AATGTCACT TGCTTAACAA ATTTGAGTCC TGCAGTTTCC TGTTTACCCC TCGATCAGTT TTCGATCACT TCCAACAACTT CCACCAAACTT CCACCAAACACTT CCCTAAGAA ATCCCCCGAA TCTCCCATTT TCTGGATACT TACCAACACAC GAACAAACTC CCCTAAGGAATA ACCCCCGGAA TCTGCCATTT TCTGGATGCT TACCAACACAG GAACAACTC CCCTAAGGAATA GATTAGCAAC CTATATACCT ATTTATAAGT CTTTGGGTT TGACCAAAACC ATCAGGAATA GATTAGCAAC CTATATACCT ATTTATAAGT CTTTGGGTT TGACCAATACA AAATTCAGG AGCCAACTCA CAATCTTTCT CAGATACTTCA GAGCCTCTCAA AAGACATTTA CCAGGATTATAA AAATTCAGG AGCCAACTCA CAATCTTTCT CAGATACTTCA GAGCCTCTCAAAA AAAAAAAAAAAAAA	5	CAAAGGCCAA ATGATCTACA TTGTTGAATC CAGTGCAATC TTGTTTTTGG GGTCACCCTG 1	680
CARTECACTE AGGGATETGE TCTTANTAGG GGAACARGC CACCARGC TGGAGGAGGA GAAGAGGTG GGGAAGCTGA AGGCTACCCT TGGAGAAGC CACCARGCC TGGAGGAGGA GAAGAAAAA ACACTAGACC TTCTGTGCTC CATATTTCC TGTGAGGTGT CTCAGCAGGT GTGGCAAGGG CAACTTGTGC AAGCCAAGCA GTTCAGCTAAT GTCACCATGC TCTCTCAGCA CATCGTTGGG TTCACTGCCA TCGCCCCCA GTGCTCACCC TGCAGGTAC TCACCATGCT CAATCCACTG TCACACCGC TCCACCAGCA GTGTGAGGAG CTGCAGTGTA TCACCATGCT GACCATTGGC GATGCCTATT GTGTAGCTG GGGATTACAC AAAGAGAGT ATCACCATGCT TGTTCAGATA GCGCTAATG CCCTGAAGAT GATGGAGCTC TCTGATCAAG TTATGTCTCC CATGGAGAA CCTATCAAGA TGCGAAATTG ACTGCACTCT GGATCAGTT TTCGGGCT CGTTGGAGAT AAAATGCCCC GTTACTGTTT TTTGGAACA AAACAGAGTT ACACATCACAC CACTGGAGAA ATCCCCCGGAA TCTGCCATTT TTGGAACA AAATGTCACTC TGGCTAACAA ATTTCAGTC TGCAGTACA TCTGCCATTT TTGGAACA AAATGTCACTC CACCAACATT CAAAGACTGT CCTGGTTTCG TGTTTACCCC TCGATCAAGG GAGGAACTT CACCAACAACT CACTGGTAAA ATCCCCCGGAA TCTGCCATTT TTGGAACAC AAACACACTC CACCAAACTT AAAACCATGC TTCCAAAAGA AAGATTTGCA AATTATACAG TATTCCAACAAG GAACAAACTC AACAGGAATA GATTAGCAAC CTAATATACCT ATTATAAAGT CTTTGCGAACTACAACAACTTCAAAGAATTCAAACACACAC		TCTCCACACA TTACAACATT TTACAACAACAACAACAACAACAACAACAACAACAACAAC	740
GAAGAGATGE GGGAAGCTGA AGCCTACCT TGAGCAAGCC CACCAAGCCC TGGAGGAGGA GAAGAAAAAA CACATAGACC TTCTGTGCTC CATATTTCCC TGTGAGGTTG CTCAGCAGCT GAGGAAGAGG CAAGTTGTG AAGCCAAGAA GTGCTCAGCAGC TCTCAGCAGC CATCGTTGGG TTCACTCCCA TCTGCTCCCA GTGCTCACCAGC CTGCAGGTCA TCACCATGC CAATCGATTGGC TACACTCGCT TCGACCAGCA GTGCTCACCC GTGCAGGTCA TCACCATGCA GACCATTGGC GATCCTATT GTGTAGCTGG GGGATTACAC GAAGAGAGA AAACAGAGTG ATACTCATGC TGTTCAGATA GCGCTGATGG CCCTGAAGAT GATGGACTC TCTGATCAGA TTTTCAGTAC TGTTCAGAAA CCTATCAAGA TGCGAATTGG AAACAGAGTT TTTCGTGGCGT CGATGGAGTT AAAATGCCCC GTTACTGCT TTTTTGGAAAC AATGTCACT TGGCTAACAA ATTTCAGTCC TGCAGTTAC CACGAAAAAT CAATGTCAGC CCAACAACTT TGCCTAACAA ATTTCAGTCC TGCAGTTAC CACGAAAAAT CAATGTCAGC CCAACAACTT CACCAACAACT CCAAGAACTG CCTGGTTTCG TGTTTACCCC TCGATCAAGG GAAGAACTT CACCACAACACT CCCTAGTAAA ATCCCCGGAA TCTGCCATTT TTTGGAAACA CACAACACTT CACCACAACACT ACCAGAAATA GATTAGCAAC CTATATACCT ATTTATAAGT CTTTGGGTT TACCACAAGA GAACACTT AAAACCATGC TCCCAAAAAA AAACATGTCAA AAACACATGC ACACAAACTC AAAACCATGC TCCCAAAAAA AAACATGTCA GAGCACTTTA AAACCATGCA GACCACTTCTA AAGCACTTTAC AGGCATTTAA AACCATTCA GACCACTTTAT AACACAACAAA ACACACTATAA AAAATTCAGG AGCCAAATCA CAATCTTTCT CTGTTTAAC ATGCACAAAA GTACTCACTT CAGTACTTCA GCCCTTCAAAA AAAAAAAAAAAAAAAAA		CANTICONOTIC ACCOMMENCA MORROLATINA CONTRACTOR CONTRACT	800
GAAGAANAG ACAGTAGACC TTCTGTGTCTC CATATTTCCC TGTGAGGTTG CTCAGGAGGT GGCGAAGGG CAAGTTGTGC AAGCAAGAA GTCAGTAAT GTCACCATGC TCTCTCTCAGA CATCGTTGGG TTCACTCCA TCTGCTCCCA GTGCTCACCG CTGCAGGTCA TCACCATGCT CAATCCACTG TACACTCGCT TCGACCAGCA GTGTGAGGAG CTGCATGTCA ACACGGTGCA GACCATTGGC GATCCCTATT GTGTAGCTGG GTGTGAGGAG CTGCATGTCA ACACGAGGTG TGTTCAGATA GCGCTGATGG CCCTGAAGAT GATGGAGCTC TCTGATGAAG TTATGTCTCC CGTTGGAGAA CCTATCAGAA TGCGAATTGG ACTGCACTCT GGATCAGTT TTCTGGCGCT CGTTGGAGT AAAATGCCC GTTACTGTCT TTTTTGGAAAC AAACTCAGTT TTCTGGCTA ATTTGAGTC TGCAGTACC CACGAAAAAAT CAATGTCACC CGACAACTT ACCACAACCTC CCCTAGTGAA ATCCCCGGAA TCTGCCCATTT TCTGGATGCT TACCACACACTC CACCAAACTT CCCTAGTGAA ATCCCCGGAA TCTGCCATTT TCTGGATGCT TACCAACAAG GACAAACTC AAAACCATGC TTCCAAAAGA AAACTGCCAACT CACCAAACTC ACACGGAATA GATTACCAACAA AAACACTTCCA AGATTGCAAACAACTC CACCAAACCTC AAAACCATGC TTCCAAAAGA AAACACTTTCA GGGATTGTAA AACTTCAGGAAACA AACCATTCACAACAAAAA AAACACTACAACAACAACTC CACCAAACACTACACAAAAAAAA		CAACACCOMO COCAACOMOA ACCOMACACA TORON TORON TORON TORON TORON	860
CRIGGRAGG CHARTISTIC ARGCCAMGA STUCACTAC CTGCAGGUA TCACCATGC CAATGCACTG TACACCCAT TCACCAGCA CTGCACCAGC CTGCAGGUA TCACCATGCT CAATGCACTG TACACTGCT TCAGACCAGCA GTGTGGACGAG CTGGAGGTCA TCACCATGCT CAATGCACTG CAATGCACTG CAATGCACATGC CTGCAAGAG CTGTGGAGAG CTGCAGAGTC AACACCATGCT TCTCAGGAA GCGCATATG GCGCTGAAGT GCGCTGAAGT AAGAGAGGTC ATACTCATGC CTGTAGAGA AAGAGAGACT TACACCATGC CTTCAAGAA CTATCAAGA TCCCCC GTACATGA AATGCACCC CTTACCAGCA AATTTCAGTC TCACCAGAAAAT CAATGCACCC CTTACATGAA AATTTCAGTC TCACAGAAAAT CAAAGACTCT CCAGGAAAAT CAAAGACTCT CCCGGATAAAA TCCCCCGAAAAAT CAAAGACTC CACCAAACACT ACACAATTCACC CCCACAAACT ACACAATTACC CCCTAGTGAA ATCCCCGGAA TCTCCCCATT TCTGGATGCT TACCAACAAG CAACCAACT CCCCTAGTGAA ATCCCCGGAA TCTCCCCTATT TCTGGATGCT TACCAACAAG CAACCAACT CCCCTAGTGAA ATCCCCGGAA TCTCCCCTATTT TCTGGATGCT TACCAACAAG CAACCAACTC CACCAAACCA CTATATACCT ATTTATAACT CCCAACAAG CAACAACTC AACACTCCAACAAACAACAACACACAACAACAACACACAACA		CAACAAAAAC AGAGTAGAGG TOTT TOTT TOTT TOTT TOTT TOT	920
CATCGTTGGG TTCACTGCCA TCGACCAGCA GTGCTCACCG CTGCAGGTCA TCACCATGCT TACACTGCT TCGACCAGCA GTGTGGAGAG CTGGAGTGTA ACAAGGTGGA GACCATTGC TACACTGCT TGCACCAGCA GTGTGGAGAG CTGGATGTCT ACAAGGTGGA GACCATTGC GACCATTGC GATGCTATG GGATTACAC AAAAGAGAGTG ATACTCATCC TGTTCAGATA GCGCTCATG GGATTACAC AAAAGAGAGTG ATACTCATCC TGTTCAGATA GCGCTCAAAAA CAATGCACTC TGGATGAGA TTATGTCTCC CCATGGAGAA CTATACAACA TGCAAATGT ACAGGACTC TTTTTGGAAAC AATGCACTT TGCCTGCGT TTTTTGGAAAC AATTCACCC TGGCTAACAA ATTTCAGTCC TCCAGTTACA CACGAAAAAT CAATGTCACC CCAACACTT TCCCAGACAACA CCAGAAAAAT CAATGTCACC CCAACACAT CCCCAAACTT CCCCTAGTGAA ATCCCCGGAA TCTGCCATT TCTGGATGAG GAGCAACACT CACCAAACT CCCAAACACT CCCAAACACAC CTATATACCA ATTTATACAC GAGCACAACT TACCAACACA AAAACACACACACACACACAC	10	CTCCCAACCC CAACTTCTCC AACCCAACAA CTTCACTCTCTCT	980
CAATGCACTG TACACTCCCT TCGACCAGCA GTGTGGAGAG CTGGATGTCT ACAAGGTGGA GACCATTGGC GATGCCTATT GTGTAGCTGG GGGATTACAC AAAAGAGAGTG ATACTCATGC TGTTCAGATA GCGCTGATGG CCCTGAAGAT GATGGAGCTC TCGATGAAG ATACTCATGC TGTTCAGATA GCGCTGATGG CCCCTAAGAT GATGGAGCTC TCGATGAAG TTATGTCTCC CCATGGAGAA CCTATCAAGA TGCGAATTG ACTGCACTT GGATCAGTT TTGGTGGGT CGTTGGAGAT AAAATGCCC GTTACCAGCT TTTTTGGAAAC AATGTCACTC TGGCTAACAA ATTTGAGTCC TGCAGTGTAC CACGAAAAAT CAATGTCAGC CCACAAACTT TGCACAAA CAAGACTGT CCTGGTTTCG TGTTTACCCC TCGATCAAG GAACAACTC CACCAAACTT CCACAGAATA ATCCCCGGAA TCTGCCATTT TCTGGATGCT TACCAACAAG GAACAAACTC CACCAAAACA AACCCTCGAA AAAACCCTTTA GGGATTGTAC TACCAACAAG GAACAAACTC AAAACCATGC TTCCAAAAGA AAGACTGTAA CAAGATGCATTA AGACATGTA AGACAATGTACT AAAATTTCAGG AGCCAAGTCA CAATCTTTCT CCGGATTACA AGCACAAACT TACCACAAAAAAAAAA		CATCCTTCCC TTCACTCCA TCTCCCA TCTCCCA CTCCCAA CTCCTCACA CTCCTCACA CTCCTCACACACA	040
GACCATTGGC GATGCCTATT TGTTCAGATA GCGCTGATGG CCCTGAAGAT GATGGAGCTC TCTGATGAAGT GATGGAGCTC TCTGATGAAGT TATGTCTCC TGTTCAGATA GCGCTGATGG CCCTGAAGAT GATGGAGCTC TCTGATGAAGT TATGTCTCC CCATGGAGAA CCTATCAGAAA TGCCAAATTGA ACTGCACTCT GGATCAGTT TTGCGGGGT ATTTGAGTCC TGCAGTGTAC CACCAAAAAT CAATGTCAGC CCAACAACTT TACGATCAA ATTGAGTCC TGCAGTGTAC CACCAAAAAT CAATGTCAGC CCAACAACTT ACAGATTACT CAAAGACTGT CCTGGTTTCG TGTTTACCCC TCGATCAAGG GAGGAACTTC CACCAAACTT CCCTAGTGAAA ATCCCCGGAA TCTGCCATTT TCTGGATGCT TACCAACAAG GAACAAACTC CCCTAGTGAA ATCCCCGGAA TCTGCCATTT TCTGGATGCT TACCAACAAG GAACAAACTC AAAACCATGC TTCCAAAAGA AAGATGTGGA AGATGGCAT GCCAATATTT TAGGCAAAGC ATCAGGAATA GATTAGCAAC CTATATACCT ATTTATAACT CTTGGGGTT TGACCTAATG AAGATCTGTA GACCATCTGA AAGACACTTTA GGGATTGTAC ATGACAAAAT GTACTCACTT CAGTACTTCA GCCCTCTGAA AAAAAAAAAA AAACCTTTAAA ATGACAAAAT GTACTCACTT CAGGATATT TAAACAGCA CTTACTACCT GTACTCAAAA TTCAGCAACTT TGTAGGATATA TCAGGATATT GTAGCAAAT GTACAAACTG ATGAGACAAAC CTGAATCTT TGTAGGATATA TCAGGATATT GTAGTCAAAT GTACAAACTG ATGAGACTACC CTGCAATCTC ATATCCTGGT GGAATGCCAT GGTTATTAAA GTGTGTTTGT GATAGTCAC CTGCAAACATCT CAAAAAAAAAA		CAATCCACTC TACACTCCCT TCCACCACCA CTCCTCCACCACCACCACCACCACCACCACCACCACCACC	100
TGTTCAGATA GCGCTGATGG CCCTGANGAT GATGGACTC TCTGATGAAG TTATGTCTCC CCATGGAGAA CCTATCANGA TGCGAATTGG ACTGCACTCT GGATCAGTTT TTGCTGGCGT CGTTGGAGTT AAAATGCCCC GTTACTGTT TTTTGGAAAC AATGTCACTC TGGCTAACAA ATTTGAGTCC TGCAGTTTCG CACCAAAAAT CAAAGACTGT CCTGGTTTCG TGTTTACCCC CCGACACACTT ACAGATTACT CACAAGACTGT CCTCGGTTTCG TGTTTACCCC CCGACACACTT ACAGATTACT CACAAGACTGT CCTCGGATTCG TGTTTACCCC CCGACACACTT ACAGAACTC CCCTAGTGAA ATCCCCGGAA TCTGCCCATTT TCTGGATGCT TACCACACAG GAACAAACTC AAAACCATGC TTCCAAAAGA AAGATCTGCA AGATGGCAAT GCCAATTTTT TAGGCAAAGC ATCAGGAATA GATTAGCAAC CTATATACCT ATTTATAACT CTTTGGGGTT TGACTCATTG AAGATCTGTA GAGCCACTCA AAGCACTTTA GGGATTGTAC AGCACATATTA CAGGTATTA AAATTTCAGG AGCCAATCA CAATCTTTCT CCTGTTTAAC ATGACAAAAT GTACCACTT CAGGTACTAA AAACCTACAA AAAAAAAAAA		CACCAMMCCC CAMCCOMAMM CMOMACOMOC GGCAMMACCA	160
CCATGGAGAA CCTATCAAGA TGCCAATTGG ACTGCACTCT GGATCAGTTT TTGCTGGCGT CGTTGGAGTT AAAATGCCCC GTTACTGTCT TTTTTGAAAC AATGTCAACT TGCTAACAA ATTTGAGTCC TGCAGTGTAC CACGAAAAAT CAATGTCAGC CCAACAACTT ACGAGTTACT CAAAGACTGC TGCAGTTTC GTTTTACCCC TGCATCAAGG GAGGAACTT CACGAAACTC CCCTAGTGAA ATCCCCGGAA TCTGCCATTT TCTGGATGCT TACCAACAAGT AAAACCATGC TTCCAAAAGA AAGATGTGGA ACATGGCAAAG GCCAAATTTT TAGGCAAAGC ATCAGGAATA GATTACCAAC CTATATACCT ATTTATAAGT CTTTGGGGTT TGACTCATTG AAGATGTGTA GAGCCTCTGA AAGCACTTTA GGGATTGAC ATGGCTAAGA ACACTGTATA AAAATTCAAGG AGCCAAGTCA CAATCTTTC CCTGTTTAAC ATGACAAAAAT GTACTCATTA AAAATTCAAGG AGCCAAGTCA CAATCTTTC CCTGTTTAAC ATGACAAAAAT GTACTCACTT CAGTACTTCA GCTCTCAAG AAAAAAAAAAAAAAAAAAA		TCTTCACATA CCCCTCATCC CCCTCAACAA CATCCACCACCACTCATA	220
CGTTGGAGTT AAAATGCCCC GTTACTGTCT TTTTGGAAAC AATGTCACTC TGGCTAACAA ATTTTGAGTCC TGCAGTGTAC CACGAAAAAT CAAATGTCAGC CCAACAACTT CAAAGACTGT CCTGGTTTCC TGTTTACCCC TGGATCAAGG GAGGACTTC CACCAAAACTT CCCTAGTGAA ATCCCCGGAA TCTGCCCATTT TCTGGATGCT TACCAACAAG GAACAAACTC TACCAGGAATA ACCAGTTTACT CCCTAGTGAA ATCCCCGGAA TCTGCCCATTT TCTGGATGCT TACCAACAAG GAACAAACTC AACACTGCAATGTCACCAACTAG CATCAGGAATA GATTACCAAC CATATTACCAACAA GAACACTTTA ATCACAGGAATA GATTACCAAC CATATTACACA AGCACTATTA AAAATTTCAGG AGCCAAGTCA CAAACTTTAC CCTGTTTAAC ATGACAAAAT GTACTCACTT TAGGGATAACA AGCAGTATTA AAAATTTCAGG AGCCATCTCAAC AAAAAAAAAA	15	CCATCCACAA CCTATCAACA TCCCAATTCCC ACTCCACTCTCC CCCACTCTCCC	
ATTTGAGTCC TGCAGTGTAC CACGAAAAAT CAATGTCAGC CCAACAACTT ACAGATTACT CAAAGACTGT CCTGGTTTCG TGTTTACCCC TCGATCAAGG GAGGAACTTC CACCAAACTT CCCCTAGTGAA ATCCCCGGAA TCTGCCAATTT TCTGAGCAAGG GAGGAACTTC CACCAAACTT ACCCAGAGGAACTG AAAACCATGC TTCCAAAAGA AAGATGTGGA AGATGGCAAT GCCAATTTT TAGCAAAGC ATCAGGAATA GATTAGCAA CCTATATACCT ATTATAAGT CTTTGGGGTT TGACTCATTG AAAATTTCAGG AGCCAAGTCA CAATCTTTCT GCGGTTTAAC ATGGCAAAAAT GTACTCACTT CAGTACTTCA GGCATCTACA AGCACTTAA AAATTTCAGG AGCCAAGTCA CAATCTTTCT CAGTACTTCA GCCATTATAAC AAAAAAAAAA		CCTTCCACTT AAATCCCCC CMMACMCM MMMMCCALAAC	280
CARAGACTET CCTGGTTTCC TGTTTACCC TGGATCARGG GAGGARCTC CACCAAACTT CCCTAGTGAA ATCCCCGGAA TCTGCCATTT TCTGGATGCT TACCAAGAG GAACACTC AAAACCATGC TTCCAAAACA AACATGTGGA AGATGGCAAT GCCAAATTTT TAGGCAAAGC ATCAGGAATA GATTAGCAAC CTATATACCT ATTTATAAGT CTTTGGGTT TGACTCATTG AAGATGTGTA GAGCCTCTGA AACCACTTTA GAGATTTTA GAGCAACACA AGCACTATTA AAATTCAGG AGCCAAGTCA CAATCTTTCT CAGGATTCTAG ATGACAACAA GCACTATTA CAGTACTTCA GCTCTTCAAG AAAAAAAAAA AAACCTTAAA AAGCTACTTT TGTGGGAGTA TTTCTATTAT ATAACCAGCA CTTACTACCT GTACTCAAAA TTCAGCACCT TGTACGATATA TCAGATAATT GTACTCAATT GATCAAACTG ATGGGTCAC CTGCAATCTC ATATCCTGGT GGAATGCCAT GGTTATTAAA GTGTGTTTGT GATAGTGTCG TCAAAAAAAAAA		ATTTGAGTCC TGCAGTGTAC CACGAAAAAT CAATGTCAGC CCAACAACTT ACACATTACTT	340
CCCTAGTGAA ATCCCCGGAA TCTGCCATTT TCTGGATGCT TACCAACAAG GAACAACTC AAAACCATGC TTCCAAAAGA AAGATGTGGA AGATGGCAAT ATCAGGAATA GATTAGCAAC CTATATACCT ATTTATAAGT CTTTGGGGTT TAGCCAACAGC AAGATGTGTA GAGCCTCTGA AAGCACTTTA GGGATTGTAG ATGGCTAACA AGCAGTATTA AAAATTCAGG AGCCAACTCA CAATCTTTCT CCTGTTTAAC ATGACAAAAT GTACTCACTT CAGGATACTCA GGTCTCTCAAG AAAAAAAAA AAACCTTAAA AAGCTACTTT TGTGGGATA TTTCTATTAT ATAACCAGCA CTTACTACCT GTACTCAAAA TCCAGCACCT TGTACAATATA TCAGGATAATT GTAGTCAATT GTACAAACTG ATGGGATCAC CTGCAATCTC ATATCCTGGT GGAATGCCAT GGTTATTAAA GTGTGTTTGT GATAGTGTCG TCAAAAAAAAAA		CAAAGACTGT CCTGGTTTCG TGTTTACCCC TCGATCAAGC CAGGAACTTC CACGAAACTT	400
AAAACCATGC TTCCAAAAGA AAGATGTGGA AGATGGCAAT GCCAATTTT TAGGCAAAGC ATCAGGAATA GATTAGCAAC CTATATACCT ATTTATAAGT CTTTGGGGTT TGACTCATTG AAGATGTGTA GAGCCTCTGA AAGCACTTTA GGGATTGTAG ATGGCTAACA AGCAGTATTA AAATTTCAGG AGCCAAGTCA CAATCTTTCT CCTGTTTAAC ATGACAAAAT GTACTCACTT CAGTACTTCA GCTCTTCAAG AAAAAAAAAA		CCCTAGTGAA ATCCCCGGAA TCTGCCATTT TCTGGATGCT TACCAACAAC CAACAAACTT	460
ATCAGGAATA GATTAGCAAC CTATATACCT ATTTATAAGT CTTTGGGGTT TGACTCATTG AAGATGTGTA GAGCCTCTGA AAGCACTTTA GGGATTGTAAC AGCAGTATTA AAAATTCAGG AGCCAAGCCA	20	AAAACCAMCC MMCCAAAACA AACAMCMCCA ACAMCCAAAA AAAAAAAA	520
AAGATGTGTA GAGCCTCTGA AAGCACTTTA GGGATTGTAG ATGGCTAACA AGCAGTATTA AAAATTTCAGG AGCCAAGTCA CAATCTTTCT CAGTACTAG AGCCAAGTCA CAATCTTTCT CAGTACTAG AGCCAAAAAAAAAA		ATCAGGAATA GATTAGCAAC CTATATACCT ATTTATAACT CTTTTCCCCTTT TCACTCATTTC	580
AAATTCAGG AGCCAAGTCA CAATCTTCT CCTGTTTAAC ATGACAAAAT GTACTACTT CAGTACTTCA GCTCTTCAAG AAAAAAAAAA AAACCTTAAA AAGCTACTTT TGTGGGAGTA TTTCTATTAT ATAACCAGCA CTTACTACCT GTACTACAAA TCAGATAATT GTAGTCAATT GTACAAACTG ATGGAGTCAC CTGCAATCTC ATATCCTGGT GGAATGCCAT GGTTATTAAA GTGTGTTTGT GATAGTGTCG TCAAAAAAAA AAAAAA AAAAAAAAAAAAAAAAAAAAA		AAGATGTGTA GAGCCTCTGA AAGCACTTTA GGCATTGTAC ATGCCTAACA AGCACTATTA	540
CACTACTTCA GCTCTTCAAC AAAAAAAAA AAACCTTAAA AAGCTACTTT TGTGGGAGTA TTTCTATTAT ATAACCAGCA CTTACTACCT GTACTCAAAA TTCAGCACCT TGTACATATA TCAGATAATT GTAGTCAATT GTACAAAACTG ATGGAGTCAC CTGCAATCTC ATATCCTGGT GGAATGCCAT GGTTATTAAA GTGTGTTGT GATAGTGTCG TCAAAAAAAAA AAAAAA AAAAAAAAAAAAAAAAAAAA		A A A TOTAL COLOR A CO	700
TTTCTATTAT ATAACCAGCA CTTACTACCT GTACTCAAAA TTCAGCACCT TGTACATATA TCAGATAATT GTAGTCAATT GTACAAACTG ATGGAGTCAC CTGCAATCTC ATATCCTGGT GGAATGCCAT GGTTATTAAA GTGTGTTTGT GATAGTGTCG TCAAAAAAAA AAAAAAAAAA		CACTACTTON COMOTIONA ANALAS ANALAS ANACOTAS	760
TCAGATAATT GTAGTCAATT GTACAAACTG ATGGAGTCAC CTGCAATCTC ATATCCTGGT GGAATGCCAT GGTTATTAAA GTGTGTTTGT GATAGTGTCG TCAAAAAAAA AAAAAAAAAA	25	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	320
GGAATGCCAT GGTTATTAAA GTGTGTTTGT GATAGTGTCG TCAAAAAAAA AAAAAAAAAA		TCAGATAATT GTAGTCAATT GTACAAACTG ATGGACTGAC GTGGAATGTG ATGGACTAGAC	380
AAAAAAAAA AAAAA 30 (2) DATA TO SEQ ID NO: 2: (i) SEQUENCE CHARACERTISTICS: (A) LENGTH: 695 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase al (hsGarain) (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 2: 5 Met Phe Cys Thr Lys Leu Lys Asp Leu Lys Ile Thr Gly Glu Cys Pro 5 10 15 Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu 20 21 22 23 24 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln 35 40 40		CCAATCCCAT CCTTATTAAA CTCTCTCTTTTCT CATACTCTCTC	940
(2) DATA TO SEQ ID NO: 2: (i) SEQUENCE CHARACERTISTICS: (A) LENGTH: 695 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase al (hscalar) (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 2: 2 Met Phe Cys Thr Lys Leu Lys Asp Leu Lys Ile Thr Gly Glu Cys Pro 5 10 15 Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu 20 25 30 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln 35 40		ΔΔΔΔΔΑΛΑ ΑΝΑΝ	000
(2) DATA TO SEQ ID NO: 2: (i) SEQUENCE CHARACERTISTICS: (A) LENGTH: 695 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase al (hsG) (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 2: 5 Met Phe Cys Thr Lys Leu Lys Asp Leu Lys Ile Thr Gly Glu Cys Pro 5 10 15 Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu 20 21 22 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln 35 40		30	015
(i) SEQUENCE CHARACERTISTICS: (A) LENGTH: 695 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase al (hsGeneral sequence) (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 2: 2 2 2 2 2 3 3 3 3 4 4 4 4 4 4 4 5 4 5 4 5 4 5 4 5	30		
(i) SEQUENCE CHARACERTISTICS: (A) LENGTH: 695 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase al (hsGeneral sequence) (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 2: 2 2 2 2 2 3 3 3 3 4 4 4 4 4 4 4 5 4 5 4 5 4 5 4 5		·	
(i) SEQUENCE CHARACERTISTICS: (A) LENGTH: 695 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase al (hsGeneral sequence) (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 2: 2 2 2 2 2 3 3 3 3 4 4 4 4 4 4 4 5 4 5 4 5 4 5 4 5		(2) DATA TO SEC ID NO. 2.	
(A) LENGTH: 695 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase al (hsG) (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 2: 25 Met Phe Cys Thr Lys Leu Lys Asp Leu Lys Ile Thr Gly Glu Cys Pro 5 10 15 Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu 20 25 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln 35 40	•	(2) Dilli 10 DDQ 1D NO. 2.	
(A) LENGTH: 695 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase al (hsG) (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 2: 25 Met Phe Cys Thr Lys Leu Lys Asp Leu Lys Ile Thr Gly Glu Cys Pro 5 10 15 Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu 20 25 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln 35 40		(i) SPONENCE CUADACEDRICATION.	
(B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase al (hsG) (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 2: 3 Met Phe Cys Thr Lys Leu Lys Asp Leu Lys Ile Thr Gly Glu Cys Pro 5 10 15 Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu 20 25 30 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln 35 40	35		
(ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase al (hsGalant) (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 2: 5 Met Phe Cys Thr Lys Leu Lys Asp Leu Lys Ile Thr Gly Glu Cys Pro 5 10 15 Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu 20 25 30 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln 35 40	-	4	
(ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase al (hsGalatin) (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 2: 45 Met Phe Cys Thr Lys Leu Lys Asp Leu Lys Ile Thr Gly Glu Cys Pro 5 10 15 Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu 20 25 30 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln 35 40		• •	
(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 2:		(b) ToroLogi: Tinear	
(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 2:		(ii) MOLEGULE MADEL	
(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 2: 45 Met Phe Cys Thr Lys Leu Lys Asp Leu Lys Ile Thr Gly Glu Cys Pro 5 10 15 Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu 20 25 30 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln 35 40	40	(11) MOLECULE TYPE: protein (human soluble guanylyl cyclase al (hsGCa	1))
Met Phe Cys Thr Lys Leu Lys Asp Leu Lys Ile Thr Gly Glu Cys Pro 5 10 15 Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu 20 25 30 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln 35 40	70		
Met Phe Cys Thr Lys Leu Lys Asp Leu Lys Ile Thr Gly Glu Cys Pro 5 10 15 Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu 20 25 30 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln 35 40	¥.		
Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu 20 25 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln 35 40		(X1) SEQUENCEDESCRIPTION: SEQ ID NO: 2:	
Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu 20 25 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln 35 40	•		
Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu 20 25 30 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln 35 40	15		
20 25 30 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln 35 40 45	40	- +0 13	
Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln 35 40 45			
35 40 45		=- 30	
The Dom The Dom Ale the second of the second	50	35 40 45	

Asp Ile Pro Glu Lys Asn Ile Gln Glu Ser Leu Pro Gln Arg Lys Thr Ser Arg Ser Arg Val Tyr Leu His Thr Leu Ala Glu Ser Ile Cys Lys Leu Ile Phe Pro Glu Phe Glu Arg Leu Asn Val Ala Leu Gln Arg Thr - 55 Leu Ala Lys His Lys Ile Lys Glu Ser Arg Lys Ser Leu Glu Arg Glu Asp Phe Glu Lys Thr Ile Ala Glu Gln Ala Val Ala Ala Gly Val Pro Val Glu Val Ile Lys Glu Ser Leu Gly Glu Glu Val Phe Lys Ile Cys

	Tyr 145	Glu	Glu	Asp	Glu	Asn 150		Leu	Gly	Val	Val 155	Gly	Gly	Thr	Leu	Lys 160
	Asp	Phe	Leu	Asn	Ser 165	Phe	Ser	Thr	Leu	Leu 170		Gln	Ser	Ser	His 175	Cys
5				180					185	Glu				190	Leu	_
	Leu	Asp	Lys 195	Glu	Asp	Asp	Phe	Leu 200	His	Val	Tyr	Tyr	Phe 205	Phe	Pro	Lys
10	Arg	Thr 210	Thr	Ser	Leu	Ile	Leu 215	Pro	Gly	Ile	Ile	Lys 220	Ala	Ala	Ala	His
	Val 222	Leu 5	Tyr	Glu	Thr	Glu 230	Val	Glu	Val	Ser	Leu 235	Met	Pro	Pro	Cys	Phe 240
	His	Asn	Asp	CÀa	Ser 245	Glu	Phe	Val	Asn	Gln 250	Pro	Tyr	Leu	Leu	Tyr 255	
15				260					265					270	Pro	
			275					280					285		Pro.	
20		290					300					305		_	Asn	-
	310					315					320				Asn	325
0.5					330					335					Phe 340	
25				345					350					355	Arg	_
			360					365					370		ГÀЗ	_
30		375					380					385			Gly	
	390					395					400				Tyr	405
35					410					415					Ile 420	_
33				425				•	430					435	Lys	
			440					445					450		ГЛа	_
40		455					460					465			Ala	
T .	470					475					480				Asn	485
45					490					495					Ser 500	
70				505					510					515	Thr	
			520					525					530		Thr	
50		535					540					545			Asp	
	550					555					560				Leu	565
55					570					575					Ile 580	
-				585					590					595	Met	
			600					605					610		Phe	
60		615					620					625			Tyr	
	Leu	11 EU	тÃэ	ush	Cys	rro	стĀ	rue	vaı	rne	Thr	Pro	Arg	Ser	Arg	Glu

630 635 640 Glu Leu Pro Pro Asn Phe Pro Ser Glu Ile Pro Gly Ile Cys His Phe 650 655 Leu Asp Ala Tyr Gln Gln Gly Thr Asn Ser Lys Pro Cys Phe Gln Lys 5 665 670 Lys Asp Val Glu Asp Gly Asn Ala Asn Phe Leu Gly Lys Ala Ser Gly Ile Asp 695

10

15

(2) DATA TO SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2443 basepairs

 - (B) TYPE: nucleotide
 (C) STRANDEDNESS: doublestrand
 (D) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

25	כככככככככ	CCCCTCCCC	CMCMCCCCCC	C=CCC=====			
20	TGCCTCCCC	CCTCCCCCCC	CTCTGCCTGG	GTCCCTTCGG	CCGTACCTCT GTGAATCACG	GCGTGGGGGC	60
	GCTGGTGATC	CCCDDTTT	CAGACACCAT	GTACGGATTT	GTGAATCACG	CCCTGGAGTT	120
	ACATCAACAA	CGCAATIACG	TOTAL CARREST	GTGGGAAGAC	ATCAAAAAAG	AGGCACAGTT	180
	CCTTCCTCCT	CCNACCNAAC	TIGICAGAAT	AATATATGAT	GACTCCAAAA	CTTATGATTT	240
30	CAACATCTTT	TTCCTCTTTTTT	CCCDACAATCT	CAATGCTGGA	GAAATCCTCC	AAATGTTTGG	300
-	CTCTAATCTC	ACACAAMMOG	GCCAAGAATC	TGGTTATGAT	ACAATCTTGC	GTGTCCTGGG	360
	CTACCCAGGA	ATCCCTCCAC	CEMCCHARLE	TGATGCTCTG	CACGACCACC	TTGCTACCAT	420
i	CATTTTTCCAC	TACTACTOCAC	CITCUITIAG	GTGCACTGAT	GCAGAAAAGG	GCAAAGGACT	480
	AACACTCCCA	CAACAAARGG	AGAGAGAAGG	ACTICAGGAT	ATTGTCATTG	GAATCATCAA	540
35	TCDACAATCT	CARCARATCC	ATGGCACTGA	AATAGACATG	AAGGTTATTC	AGCAAAGAAA	600
•	TTATCARCAT	CTTCACACACA	MATTITIAAT	TGAAGAAAA	GAGTCAAAAG	AAGAGGATTT	660
	TACATTCTCC	AAACCOODOO	TTGAAGAAAA	TGGTACCCAG	GAATCACGCA	TCAGCCCATA	720
	GTGTGGCAAT	COTATATATA	CATTTCATAT	AATATTTGAC	CGGGACCTAG	TGGTCACTCA	780
	GTGTGGCAAT	TCCCTCCTTCC	GAGTTCTCCC	CCAGCTCCAG	CCTGGGAATT	GCAGCCTTCT	840
40	CATCALCITC	COMMONOGRAM	GTCCTCATAT	TGATATTAGT	TTCCATGGGA	TCCTTTCTCA	900
10	VACACY CCV A	GITTITGTAT	TGAGAAGCAA	GGAAGGATTG	TTGGATGTGG	AGAAATTAGA	960
w.	CONCORNACION	GAACTGACTG	GGACTGAGAT	CAGCTGCTTA	CGTCTCAAGG	GTCAAATGAT	1020
	CCATTTACCT	GAAGCAGATA	GCATACTTTT	TCTATGTTCA	CCAAGTGTCA	TGAACCTGGA	1080
•	TCTTCTTCTT	AGGAGAGGGC	TGTATCTAAG	TGACATCCCT	CTGCATGATG	CCACGCGCGA	1140
45	CCTCACTCAC	TIGGGAGAAC	AATTTAGAGA	GGAATACAAA	CTCACCCAAG	AACTGGAAAT	1200
70	CACAMECONC	AGGCTACAGC	TCACGTTAAG	AGCCCTGGAA	GATGAAAAGA	AAAAGACAGA	1260
	ACTOCOCTOCOC	TATTCTGTCC	TTCCTCCGTC	TGTTGCCAAT	GAGCTGCGGC	ACAAGCGTCC	1320
	MCCMmmcmcm	AAAAGATATG	ACAATGTGAC	CATCCTCTTT	AGTGGCATTG	TGGGCTTCAA	1380
	CCACCOCCA	AGCAAGCATG	CATCTGGAGA	AGGAGCCATG	AAGATCGTCA	ACCTCCTCAA	1440
50	CGMCCTCTAC	ACCAGATTTG	ACACACTGAC	TGATTCCCGG	AAAAACCCAT	TTGTTTATAA	1500
50	GGTGGAGACT	GTTGGTGACA	AGTATATGAC	AGTGAGTGGT	TTACCAGAGC	CATGCATTCA	1560
	CCATGCACGA	TCCATCTGCC	ACCTGGCCTT	GGACATGATG	GAAATTGCTG	GCCAGGTTCA	1620
	AGTAGATGGT	GAATCTGTTC	AGATAACAAT	AGGGATACAC	ACTGGAGAGG	TAGTTACAGG	1680
	TGTCATAGGA	CAGCGGATGC	CTCGATACTG	TCTTTTTGGG	AATACTGTCA	ACCTCACAAG	1740
55	CCGAACAGAA	ACCACAGGAG	AAAAGGGAAA	AATAAATGTG	TCTGAATATA	CATACAGATG	1800
JJ	TCTTATGTCT	CCAGAAAATT	CAGATCCACA	ATTCCACTTG	GAGCACAGAG	GCCCAGTGTC	1860
	CATGAAGGGC	AAAAAAGAAC	CAATGCAAGT	TTGGTTTCTA	TCCAGAAAA	ATACAGGAAC	1920
	AGAGGAAACA	AAGCAGGATG	ATGACTGAAT	CTTGGATTAT	GGGGTGAAGA	GGAGTACAGA	1980
	CTAGGTTCCA	GTTTTCTCCT	AACACGTGCC	AAGCCCAGGA	GCAGTTCTTC	CCTATGGATA	2040
60	CAGATTTTCT	TTTGTCCTTG	TCCATTACCC	CAAGACTTTC	TTCTAGATAT	ATCTCTCACT	2100
60	ATCCGTTATT	CAACCTTAGC	TCTGCTTTCT	ATTACTTTTT	AGGCTTTAGT	ATATTATCTA	2160
	AAGTTTGGCT	TTTGATGTGG	ATGATGTGAG	CTTCATGTGT	CTTAAAATCT	ACTACAAGCA	2220

(2) DATA TO SEQ ID NO: 4: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 619 amino acids (B) TYPE: amino acids (B) TYPE: mino acid (B) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase b1 (hsgCb1) (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 4: 20 Met Tyr Gly Phe Val Asn His Ala Leu Glu Leu Leu Val Ile Arg Asn (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 4: 20 Met Tyr Gly Phe Val Asn His Ala Leu Glu Leu Leu Val Ile Arg Asn (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 4: 20 Met Tyr Gly Phe Val Asn His Ala Leu Glu Leu Leu Val Ile Arg Asn (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 4: 20 Met Tyr Gly Phe Val Asn His Ala Leu Glu Leu Leu Val Ile Arg Asn (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 4: 20 Met Tyr Gly Phe Val Asn His Ala Leu Glu Leu Leu Val Ile Arg Asn (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 4: 20 Met Tyr Gly Phe Val Asn His Ala Leu Glu Leu Leu Val Ile Arg Asn (a) Seq Glu Gly Glu Phe Leu Val Arg Ile Ile Tyr Asp Asp Ser Lys Thr 40 45 40 45 31 50 32 Ser Gly Tyr Asp His Leu Holly Leu Asn Leu Asn Ala Gly 55 60 40 Ile Leu Gln Met Phe Gly Lys Met Phe Phe Val Phe Cys Gln Glu 65 70 30 Ser Gly Tyr Asp Thr Ile Leu Arg Val Leu Gly Ser Asn Val Arg Glu 65 95 60 Phe Leu Gln Asn Leu Asp Ala Leu His Asp His Leu Ala Thr Ile Tyr 100 105 Pro Gly Met Arg Ala Pro Ser Phe Arg Cys Thr Asp Ala Glu Lys Gly 115 125 Lys Gly Leu Ile Leu His Tyr Tyr Ser Glu Arg Glu Gly Leu Gln Asp 130 125 140 126 140 126 Asp Met Lys Val Ile Gln Gln Arg Asn Glu Glu Cys Asp His 141 142 40 Glu Ile Asp Met Lys Val Ile Gln Gln Arg Asn Glu Glu Cys Asp His 142 120 143 120 120 144 120 Arg Asp Clu Jan Ala Fle Tyr Arg Val Leu 245 200 246 200 257 200 258 200 259 200 260 265 260 265 275 200 280 215 280 220 Arg Asp Leu Val Val Thr Gln Cys Gly Asn Ala Ile Tyr Arg Val Leu 245 220 Arg Asp Leu Asp Arg Phe Glu Glu Arg Cys Thr Glu Glu Asp Phe Tyr 220 240 241 Arg Pro His Ile Asp Ile Ser Phe His Gly Thr Gln Glu Ser His Ile 270 280 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu 305 305 310 305 310 305 310 305 310 3	5	AAA: TAG:	TGAA TGTT	ACT CCA	GAAC	AGTG TATG	T TT:	GGCC ATGT	ATGI ATAI	G TA	TATI 'AATG	TATA ACTA	TAA	TGTT TGTA	TAC	CAAA	TTAGTT TCTGTT	2280 2340 2400 2443
(a) LENGTH: 619 amino acids (B) TYPE: anino acid (C) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase bl (hsGCbl) (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 4: 20 Met Tyr Gly Phe Val Asn His Ala Leu Glu Leu Leu Val Ile Arg Asn 5 10 15 Tyr Gly Pro Glu Val Trp Glu Asp Ile Lys Lys Glu Ala Gln Leu Asp 20 25 25 30 Clu Glu Gly Gln Phe Leu Val Arg Ile Ile Tyr Asp Asp Ser Lys Thr 40 40 4 Asp Asp Asp He Leu Val Arg Ile Ile Tyr Asp Asp Ser Lys Thr 50 Glu Ile Leu Gln Met Phe Gly Lys Met Phe Phe Val Phe Cys Gln Glu 61 Ile Leu Gln Met Phe Gly Lys Met Phe Phe Val Phe Cys Gln Glu 63 Ser Gly Tyr Asp Thr Ile Leu Arg Val Leu Gly Ser Asn Val Arg Glu 65 Phe Leu Gln Asn Leu Asp Ala Leu His Asp His Leu Ala Thr Ile Tyr 100 105 105 Pro Gly Met Arg Ala Pro Ser Phe Arg Cys Thr Asp Ala Glu Lys Gly 115 Lys Gly Leu Ile Leu His Tyr Tyr Ser Glu Arg Glu Gly Leu Gln Asp 130 135 Ile Val Ile Gly Ile Ile Lys Thr Val Ala Gln Gln Ile His Gly Thr 145 40 Glu Ile Asp Met Lys Val Ile Gln Gln Arg Asn Glu Glu Cys Asp His 106 Glu Ile Asp Leu Asp Arg Phe Glu Glu Asn Gly Thr Gln Glu Ser Arg Ile 207 Ser Pro Tyr Thr Phe Cys Lys Ala Phe Pro Phe His Ile Ile Phe Asp 210 225 Arg Asp Leu Val Val Thr Gln Cys Gly Asn Gly Thr Gln Glu Ser Arg Ile 226 Asn Thr Val Phe Val Leu Arg Ser Leu Leu Ser Val Phe Ser Leu 227 230 235 Lys Leu Glu Cys Glu Asp Glu Gly Leu Leu Ser Val Cu 245 Val Arg Pro His Ile Asp Ile Ser Phe His Gly Ile Leu Ser His Ile 227 238 Arg Leu Lys Gly Gln Asp Glu Leu Thr Gly Thr Glu Glu Ser Cys Leu 240 241 242 243 240 245 Val Arg Pro His Ile Asp Ile Ser Phe His Gly Leu Leu Asp Val Glu 245 240 241 245 240 246 247 240 247 240 247 240 247 240 247 240 240 247 240 240 245 240 240 245 240 240 245 240 240 245 240 247 240 240 245 240 240 245 240 240 245 240 240 245 240 240 245 240 240 245 240 240 245 240 240 245 240 240 245 240 240 245 240 240 245 240 240 245 240 240 245 240 240 245 240 240 241 245 240 240 245 240 240 241 245 240 240 241 245 240 240 245 240 240 245 240 240 245 240 240 240 245 240 240 240 245 240 240 245 240 24		(2)	DAT	A TO	SEQ	ID	NO:	4:										
(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 4: 20 Met Tyr Gly Phe Val Asn His Ala Leu Glu Leu Leu Val Ile Arg Asn 10 15 Tyr Gly Pro Glu Val Trp Glu Asp Ile Lys Lys Glu Ala Gln Leu Asp 20 25 Glu Glu Gly Gln Phe Leu Val Arg Ile Ile Tyr Asp Asp Ser Lys Thr 35 Tyr Asp Leu Val Ala Ala Ala Ser Lys Val Leu Asn Leu Asn Ala Gly 50 60 Glu Ile Leu Gln Met Phe Gly Lys Met Phe Phe Val Phe Cys Gln Glu 65 70 75 80 Ser Gly Tyr Asp Thr Ile Leu Arg Val Leu Gly Ser Asn Val Arg Glu 85 90 Phe Leu Gln Asn Leu Asp Ala Leu His Asp His Leu Ala Thr Ile Tyr 100 105 Pro Gly Met Arg Ala Pro Ser Phe Arg Cys Thr Asp Ala Glu Lys Gly 115 Lys Gly Leu Ile Leu His Tyr Tyr Ser Glu Arg Glu Gly Leu Gln Asp 130 Ile Val Ile Gly Ile Ile Lys Thr Val Ala Gln Gln Ile His Gly Thr 145 150 155 160 Glu Ile Asp Met Lys Val Ile Gln Gln Asp Asn Glu Glu Cys Asp His 165 Thr Gln Phe Leu Ile Glu Glu Lys Glu Ser Lys Glu Glu Asp Phe Tyr 180 Glu Asp Leu Asp Arg Phe Glu Glu Asn Gly Glu Glu Asp Phe Tyr 180 Glu Asp Leu Asp Arg Phe Glu Glu Asn Gly Thr Gln Gls Ser Arg Ile 205 Ser Pro Tyr Thr Phe Cys Lys Ala Phe Pro Phe His Ile Ile Phe Asp 210 Arg Asp Leu Val Val Thr Gln Cys Gly Asn Ala Ile Tyr Arg Val Leu 225 Arg Asp Leu Val Val Thr Gln Cys Gly Asn Ala Ile Tyr Arg Val Leu 226 Val Arg Pro His Ile Asp Ile Ser Phe His Gly Ile Leu Ser Leu 227 Val Arg Pro His Ile Asp Ile Ser Phe His Gly Ile Leu Ser Leu 226 Asn Thr Val Phe Val Leu Arg Ser Lys Glu Gly Leu Leu Asp Val Glu 227 Asn Thr Val Phe Val Leu Arg Ser Lys Glu Gly Leu Leu Asp Val Glu 290 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu 320 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu 320 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu 320 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu 320 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu 320	10		(i	(A (B) LE) TY	ngth Pe :	: 61 amin	9 am o ac	ino id		s							
20 Met Tyr Gly Phe Val Asn His Ala Leu Glu Leu Leu Val Ile Arg Asn 5	15		(ii) MO	LECU	LE T	YPE:	pro	tein	(hu	man	solu	ble	guan	ylyl	cyc	lase b1	(hsGCb1))
Tyr Gly Pro Glu Val Trp Glu Asp Ile Lys Lys Glu Ala Gln Leu Asp 20 21 25 30 30 31 35 35 37 38 38 39 30 30 30 30 30 30 30 30 31 35 35 37 37 38 38 39 30 30 30 30 30 30 30 30 30 30 30 30 30			(xi) SE	QUEN	CEDE	SCRI:	PTIO	N: S	EQ I	D NO	: 4:						
Tyr Gly Pro Glu Val Trp Glu Asp Ile Lys Lys Glu Ala Gln Leu Asp 20 20 21 25 30 30 30 30 30 30 30 30 30 30 30 30 30	20	Met	туг	Gly	Phe		Asn	His	Ala	Leu		Leu	Leu	Val	Ile		Asn	
25 Glu Glu Gly Gln Phe Leu Val Arg Ile Ile Tyr Asp Asp Ser Lys Thr		Tyr	Gly	Pro	Glu	_	Trp	Glu	Asp			Lys	Glu	Ala		Leu	Asp	
Tyr Asp Leu Val Ala Ala Ala Ser Lys Val Leu Asn Leu Asn Ala Gly 50 51 52 61u Ile Leu Gln Met Phe Gly Lys Met Phe Phe Val Phe Cys Gln Glu 65 70 75 80 30 Ser Gly Tyr Asp Thr Ile Leu Arg Val Leu Gly Ser Asn Val Arg Glu 95 Phe Leu Gln Asn Leu Asp Ala Leu His Asp His Leu Ala Thr Ile Tyr 100 105 106 Pro Gly Met Arg Ala Pro Ser Phe Arg Cys Thr Asp Ala Glu Lys Gly 115 120 120 125 Lys Gly Leu Ile Leu His Tyr Tyr Ser Glu Arg Glu Gly Leu Gln Asp 130 11e Val Ile Gly Ile Ile Lys Thr Val Ala Gln Gln Ile His Gly Thr 145 150 160 Glu Ile Asp Met Lys Val Ile Gln Gln Arg Asn Glu Glu Cys Asp His 165 170 180 185 Thr Gln Phe Leu Ile Glu Glu Lys Glu Ser Lys Glu Glu Asp Phe Tyr 180 Ser Pro Tyr Thr Phe Cys Lys Ala Phe Pro Phe His Ile Ile Feh Asp 210 Arg Asp Leu Val Val Thr Gln Cys Gly Asn Ala Ile Tyr Arg Val Leu 225 Val Arg Pro His Ile Asp Ile Ser Phe His Gly Ile Leu Ser His Ile 260 270 Asn Thr Val Phe Val Leu Arg Ser Lys Glu Gly Leu Leu Ser His Ile 260 270 Asn Thr Val Phe Val Leu Arg Ser Lys Glu Gly Leu Leu Asp Val Glu 275 Lys Leu Glu Cys Glu Asp Glu Leu Thr Gly Thr Glu Ile Ser Cys Leu 290 Arg Leu Lys Gly Gln Met Ile Var Leu Pro Glu Ala Asp Ser Ile Leu 305 310 310 315	25	Glu	Glu	Gly		Phe	Leu	Val			Ile	Tyr	Asp	Asp	30 Ser	Lys	Thr	
Glu Ile Leu Gln Met Phe Gly Lys Met Phe Phe Val Phe Cys Gln Glu 65	20	Tyr	Asp		Val	Ala	Ala	Ala		Lys	Val	Leu	Asn		Asn	Ala	Gly	
Ser Gly Tyr Asp Thr Ile Leu Arg Val Leu Glu Ser Asn Val Arg Glu 85 Phe Leu Gln Asn Leu Asp Ala Leu His Asp His Leu Ala Thr Ile Tyr 100 100 105 Pro Gly Met Arg Ala Pro Ser Phe Arg Cys Thr Asp Ala Glu Lys Gly 115 Lys Gly Leu Ile Leu His Tyr Tyr Ser Glu Arg Glu Gly Leu Gln Asp 130 11e Val Ile Gly Ile Ile Lys Thr Val Ala Gln Gln Ile His Gly Thr 145 Glu Ile Asp Met Lys Val Ile Gln Gln Arg Asn Glu Glu Cys Asp His 165 Thr Gln Phe Leu Ile Glu Glu Lys Glu Ser Lys Glu Glu Asp Phe Tyr 180 Glu Asp Leu Asp Arg Phe Glu Glu Asn Gly Thr Gln Glu Ser Arg Ile 200 Ser Pro Tyr Thr Phe Cys Lys Ala Phe Pro Phe His Ile Ile Phe Asp 210 Arg Asp Leu Val Val Thr Gln Cys Gly Asn Ala Ile Tyr Arg Val Leu 225 Pro Gln Leu Gln Pro Gly Asn Cys Ser Leu Leu Ser Val Phe Ser Leu 226 Val Arg Pro His Ile Asp Ile Ser Phe His Gly Ile Leu Asp Val Glu 255 Val Arg Pro His Ile Asp Glu Leu Arg Ser Lys Glu Gly Leu Leu Asp Val Glu 280 Asg Leu Glu Cys Glu Asp Glu Leu Thr Gly Thr Glu Ile Ser Cys Leu 290 Arg Leu Glu Cys Glu Asp Glu Leu Thr Gly Thr Glu Ile Ser Cys Leu 290 Arg Leu Cys Glu Asp Glu Leu Thr Gly Thr Glu Ile Ser Cys Leu 290 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu 305		Glu		Leu	Gln	Met	Phe		Lys	Met	Phe	Phe		Phe	Cys	Gln	Glu	
Phe Leu Gln Asn Leu Asp Ala Leu His Asp His Leu Ala Thr The Tyr	30	65					70					75					80	
100						85					90					95		
Lys Gly Leu Ile Leu His Tyr Tyr Ser Glu Arg Glu Gly Leu Gln Asp 130 135 140 Ile Val Ile Gly Ile Ile Lys Thr Val Ala Gln Gln Ile His Gly Thr 145 150 150 155 160 Glu Ile Asp Met Lys Val Ile Gln Gln Arg Asn Glu Glu Cys Asp His 165 165 Thr Gln Phe Leu Ile Glu Glu Lys Glu Ser Lys Glu Glu Asp Phe Tyr 180 185 190 Glu Asp Leu Asp Arg Phe Glu Glu Asn Gly Thr Gln Glu Ser Arg Ile 200 Ser Pro Tyr Thr Phe Cys Lys Ala Phe Pro Phe His Ile Ile Phe Asp 210 Arg Asp Leu Val Val Thr Gln Cys Gly Asn Ala Ile Tyr Arg Val Leu 225 Pro Gln Leu Gln Pro Gly Asn Cys Ser Leu Leu Ser Val Phe Ser Leu 245 Val Arg Pro His Ile Asp Ile Ser Phe His Gly Ile Leu Ser His Ile 260 Asn Thr Val Phe Val Leu Arg Ser Lys Glu Gly Leu Leu Asp Val Glu 290 Arg Leu Cys Glu Asp Glu Leu Thr Gly Thr Glu Ile Ser Cys Leu 290 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu 305 310 310 320					100					105					110			
130	35			115					120					125			-	
145			130					135					140				_	
40 Glu Ile Asp Met Lys Val Ile Gln Gln Arg Asn Glu Glu Cys Asp His 165 Thr Gln Phe Leu Ile Glu Glu Lys Glu Ser Lys Glu Glu Asp Phe Tyr 180 Glu Asp Leu Asp Arg Phe Glu Glu Asn Gly Thr Gln Glu Ser Arg Ile 200 Ser Pro Tyr Thr Phe Cys Lys Ala Phe Pro Phe His Ile Ile Phe Asp 210 Arg Asp Leu Val Val Thr Gln Cys Gly Asn Ala Ile Tyr Arg Val Leu 225 Val Arg Pro His Ile Asp Ile Ser Phe His Gly Ile Leu Ser His Ile 260 Asn Thr Val Phe Val Leu Arg Ser Lys Glu Gly Ile Leu Ser His Ile 290 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Asp Ser Ile Leu 305 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Asp Ser Ile Leu 315 320		Ile 145	Val	Ile	Gly	Ile	Ile 150	Lys	Thr	Val	Ala		Gln	Ile	His	Gly		
Thr Gln Phe Leu Ile Glu Glu Lys Glu Ser Lys Glu Glu Asp Phe Tyr 180	40	Glu	Ile	Asp	Met	Lys	Val	Ile	Gln	Gln	Arg	Asn	Glu	Glu	Сув	Asp	His	
Glu Asp Leu Asp Arg Phe Glu Glu Asn Gly Thr Gln Glu Ser Arg Ile 195	₩ .	Thr	Gln	Phe	Leu 180	Ile	Glu	Glu	Lys	Glu	Ser	Lys	Ğlu	Glu		Phe	Tyr	
Ser Pro Tyr Thr Phe Cys Lys Ala Phe Pro Phe His Ile Ile Phe Asp 210 Arg Asp Leu Val Val Thr Gln Cys Gly Asn Ala Ile Tyr Arg Val Leu 225 Pro Gln Leu Gln Pro Gly Asn Cys Ser Leu Leu Ser Val Phe Ser Leu 250 Val Arg Pro His Ile Asp Ile Ser Phe His Gly Ile Leu Ser His Ile 260 Asn Thr Val Phe Val Leu Arg Ser Lys Glu Gly Leu Leu Asp Val Glu 275 Lys Leu Glu Cys Glu Asp Glu Leu Thr Gly Thr Glu Ile Ser Cys Leu 290 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu 305	45	Glu	Asp	Leu		Arg	Phe	Glu	Glu		Gly	Thr	Gln		Ser	Arg	Ile	
Arg Asp Leu Val Val Thr Gln Cys Gly Asn Ala Ile Tyr Arg Val Leu 225 230 240 Pro Gln Leu Gln Pro Gly Asn Cys Ser Leu Leu Ser Val Phe Ser Leu 255 255 Val Arg Pro His Ile Asp Ile Ser Phe His Gly Ile Leu Ser His Ile 260 265 270 Asn Thr Val Phe Val Leu Arg Ser Lys Glu Gly Leu Leu Asp Val Glu 275 Lys Leu Glu Cys Glu Asp Glu Leu Thr Gly Thr Glu Ile Ser Cys Leu 290 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu 305		Ser	Pro		Thr	Phe	Cys	Lys		Phe	Pro	Phe			Ile	Phe	Asp	
50 Pro Gln Leu Gln Pro Gly Asn Cys Ser Leu Leu Ser Val Phe Ser Leu 245 250 255 Val Arg Pro His Ile Asp Ile Ser Phe His Gly Ile Leu Ser His Ile 260 265 270 Asn Thr Val Phe Val Leu Arg Ser Lys Glu Gly Leu Leu Asp Val Glu 275 Lys Leu Glu Cys Glu Asp Glu Leu Thr Gly Thr Glu Ile Ser Cys Leu 290 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu 305 310 320		Arg		Leu	Val	Val			Cys	Gly	Asn	Ala	220 Ile	Tyr	Arg	Val	Leu	
Val Arg Pro His Ile Asp Ile Ser Phe His Gly Ile Leu Ser His Ile 260 255 Asn Thr Val Phe Val Leu Arg Ser Lys Glu Gly Leu Leu Asp Val Glu 275 Lys Leu Glu Cys Glu Asp Glu Leu Thr Gly Thr Glu Ile Ser Cys Leu 290 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu 305 255 256 270 Asp Val Glu 280 285 Lys Leu Glu Cys Glu Asp Glu Leu Thr Gly Thr Glu Ile Ser Cys Leu 290 300 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu 305	50		Gln	Leu	Gln	Pro		Asn	Cys	Ser	Leu	235 Leu	Ser	Val	Phe	Ser	240 Leu	
Asn Thr Val Phe Val Leu Arg Ser Lys Glu Gly Leu Leu Asp Val Glu 275 Lys Leu Glu Cys Glu Asp Glu Leu Thr Gly Thr Glu Ile Ser Cys Leu 290 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu 305 310 320	-					245					250					255		
Lys Leu Glu Cys Glu Asp Glu Leu Thr Gly Thr Glu Ile Ser Cys Leu 290 295 300 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu 305 310 315 320					260					265					270			
290 295 300 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu 305 310 315 320	55			275					280					285				
305 310 315 320			290					295					300					
6U Phe Leu Cys Ser Pro Ser Val Met Asn Lou Asn Asn Tou Man Tou The Transfer		305					310					315					320	
325 330 335	60	Phe :	Leu	Cys	Ser	Pro 325	Ser	Val	Met	Asn		Asp	Asp	Leu	Thr		Arg	

```
Gly Leu Tyr Leu Ser Asp Ile Pro Leu His Asp Ala Thr Arg Asp Leu
                                      345
     Val Leu Leu Gly Glu Gln Phe Arg Glu Glu Tyr Lys Leu Thr Gln Glu
                                  360
                                                      365
     Leu Glu Ile Leu Thr Asp Arg Leu Gln Leu Thr Leu Arg Ala Leu Glu
                             375
                                                  380
     Asp Glu Lys Lys Lys Thr Asp Thr Leu Leu Tyr Ser Val Leu Pro Pro
                         390
                                              395
     Ser Val Ala Asn Glu Leu Arg His Lys Arg Pro Val Pro Ala Lys Arg
10
                     405
                                         410
     Tyr Asp Asn Val Thr Ile Leu Phe Ser Gly Ile Val Gly Phe Asn Ala
                 420
                                     425
     Phe Cys Ser Lys His Ala Ser Gly Glu Gly Ala Met Lys Ile Val Asn
             435
                                 440
                                                      445
15
     Leu Leu Asn Asp Leu Tyr Thr Arg Phe Asp Thr Leu Thr Asp Ser Arg
                             455
                                                  460
     Lys Asn Pro Phe Val Tyr Lys Val Glu Thr Val Gly Asp Lys Tyr Met
                         470
                                             475
     Thr Val Ser Gly Leu Pro Glu Pro Cys Ile His His Ala Arg Ser Ile
20
                     485
                                         490
     Cys His Leu Ala Leu Asp Met Met Glu Ile Ala Gly Gln Val Gln Val
                 500
                                     505
     Asp Gly Glu Ser Val Gln Ile Thr Ile Gly Ile His Thr Gly Glu Val
             515
                                 520
                                                      525
25
     Val Thr Gly Val Ile Gly Gln Arg Met Pro Arg Tyr Cys Leu Phe Gly
                             535
                                                  540
     Asn Thr Val Asn Leu Thr Ser Arg Thr Glu Thr Thr Gly Glu Lys Gly
                         550
     Lys Ile Asn Val Ser Glu Tyr Thr Tyr Arg Cys Leu Met Ser Pro Glu
30
                     565
                                         570
     Asn Ser Asp Pro Gln Phe His Leu Glu His Arg Gly Pro Val Ser Met
                                     585
     Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn
             595
35
     Thr Gly Thr Glu Glu Thr Lys Gln Asp Asp
         610
                             615
     (2) DATA TO SEQ ID NO: 5:
40
       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 14 amino acids
              (B) TYPE: amino acid
              (D) TOPOLOGY: linear
45
         (ii) MOLECULE TYPE: peptide (amino acids 634-647 of hsGCal)
         (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 5:
50
     Phe Thr Pro Arg Ser Arg Glu Glu Leu Pro Pro Asn Phe Pro
     (2) DATA TO SEQ ID NO: 6:
55
          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 22 amino acids
              (B) TYPE: amino acid
              (D) TOPOLOGY: linear
60
```

(ii) MOLECULE TYPE: peptide (amino acids 593-614 of hsGCb1)

```
(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 6:
 5
      Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn
                                            10
      Thr Gly Thr Glu Glu Thr
                   20
10
      (2) DATA TO SEQ ID NO: 7:
           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 28 basepairs
                (B) TYPE: nucleotide
15
                (C) STRANDEDNESS: single strans
                (D) TOPOLOGY: linear
          (ii) MOLECULE TYPE: genomic DNA
20
         (iii) HYPOTHETICAL: no
          (iv) ANTISENSE: no
25
          (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 7:
     AAAAGGATCC ATGTTCTGCA CGAAGCTC
                                                                                 28
30
     2) DATA TO SEQ ID NO: 8:
           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 18 basepairs
35
                (B) TYPE: nucleotide
                (C) STRANDEDNESS: single strans
                (D) TOPOLOGY: linear
          (ii) MOLECULE TYPE: genomic DNA
40
         (iii) HYPOTHETICAL: no
          (iv) ANTISENSE: no
45
          (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 8:
     ATTATGGAAG CAGGGAGG
                                                                                 18
50
     2) DATA TO SEQ ID NO: 9:
           (i) SEQUENCE CHARACTERISTICS:
55
                (A) LENGTH: 28 basepairs
                (B) TYPE: nucleotide
                (C) STRANDEDNESS: single strans
                (D) TOPOLOGY: linear
60
         (ii) MOLECULE TYPE: genomic DNA
        (iii) HYPOTHETICAL: no
```

	(IV) ANTISENSE: NO	
5	(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 9:	
	AAAAGGATCC ATGTACGGAT TTGTGAAT	28
10	2) DATA TO SEQ ID NO: 10:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 basepairs (B) TYPE: nucleotide (C) STRANDEDNESS: single strans (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: genomic DNA	
20	(iii) HYPOTHETICAL: no	
	(iv) ANTISENSE: no	
25	(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 10:	
	ATGCGTGATT CCTGGGTACC	20